



OIPE

RAW SEQUENCE LISTING

DATE: 01/16/2002

PATENT APPLICATION: US/10/032,254

TIME: 18:43:55

Input Set : A:\M-2335pl.app

Output Set: N:\CRF3\01162002\J032254.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: CHODOSH, Lewis
 4 GARDNER, H
 6 <120> TITLE OF INVENTION: PREGNANCY UP-REGULATED, NONUBIQUITOUS CaM KINASE
 8 <130> FILE REFERENCE: 22253-70422
 10 <140> CURRENT APPLICATION NUMBER: US/10/032,254
 11 <141> CURRENT FILING DATE: 2001-12-21
 13 <150> PRIOR APPLICATION NUMBER: 60/257,073
 14 <151> PRIOR FILING DATE: 2000-12-21
 16 <160> NUMBER OF SEQ ID NOS: 8
 18 <170> SOFTWARE: PatentIn Ver. 2.1
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 21 <211> LENGTH: 1554
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Murinae gen. sp.
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 29 tctctgaggt gatgctggcc caggaaaggg gctctgctca tcttggtggc ctcaagtgc 240
 30 ttcccaagaa agcacttcgg ggcaaggagg ccctggtgga gaatgagatc gcggtacttc 300
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 33 gctcctacac agagaaggac gccagccacc ttgtagggca ggtccttggc gctgtctcct 480
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 37 agaaacccta cggaaggcc gtagatgtgt gggccctggg tgtcatctcc tacatcctgc 720
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 55 <211> LENGTH: 343

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56 <212> TYPE: PRT
57 <213> ORGANISM: Murinae gen. sp.
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64           20           25           30
66 Gln Glu Arg Gly Ser Ala His Leu Val Ala Leu Lys Cys Ile Pro Lys
67   35           40           45
69 Lys Ala Leu Arg Gly Lys Glu Ala Leu Val Glu Asn Glu Ile Ala Val
70   50           55           60
72 Leu Arg Arg Ile Ser His Pro Asn Ile Val Ala Leu Glu Asp Val His
73   65           70           75           80
75 Glu Ser Pro Ser His Leu Tyr Leu Ala Met Glu Leu Val Thr Gly Gly
76           85           90           95
78 Glu Leu Phe Asp Arg Ile Met Glu Arg Gly Ser Tyr Thr Glu Lys Asp
79   100          105          110
81 Ala Ser His Leu Val Gly Gln Val Leu Gly Ala Val Ser Tyr Leu His
82   115          120          125
84 Ser Leu Gly Ile Val His Arg Asp Leu Lys Pro Glu Asn Leu Leu Tyr
85   130          135          140
87 Ala Thr Pro Phe Glu Asp Ser Lys Ile Met Val Ser Asp Phe Gly Leu
88  145          150          155          160
90 Ser Lys Ile Gln Ala Gly Asn Met Leu Gly Thr Ala Cys Gly Thr Pro
91           165          170          175
93 Gly Tyr Val Ala Pro Glu Leu Leu Glu Gln Lys Pro Tyr Gly Lys Ala
94   180          185          190
96 Val Asp Val Trp Ala Leu Gly Val Ile Ser Tyr Ile Leu Leu Cys Gly
97   195          200          205
99 Tyr Pro Pro Phe Tyr Asp Glu Ser Asp Pro Glu Leu Phe Ser Gln Ile
100  210          215          220
102 Leu Arg Ala Ser Tyr Glu Phe Asp Ser Pro Phe Trp Asp Asp Ile Ser
103 225          230          235          240
105 Glu Ser Ala Lys Asp Phe Ile Arg His Leu Leu Glu Arg Asp Pro Gln
106           245          250          255
108 Lys Arg Phe Thr Cys Gln Gln Ala Leu Gln His Leu Trp Ile Ser Gly
109           260          265          270
111 Asp Ala Ala Phe Asp Arg Asp Ile Leu Gly Ser Val Ser Glu Gln Ile
112           275          280          285
114 Gln Lys Asn Phe Ala Arg Thr His Trp Lys Arg Ala Phe Asn Ala Thr
115           290          295          300
117 Ser Phe Leu Arg His Ile Arg Lys Leu Gly Gln Ser Pro Glu Gly Glu
118 305          310          315          320
120 Glu Ala Ser Arg Gln Cys Met Thr Arg His Ser His Pro Gly Leu Gly
121           325          330          335
123 Thr Ser Gln Ser Pro Lys Trp
124           340
127 <210> SEQ ID NO: 3
128 <211> LENGTH: 21

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DATE: 01/16/2002

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Input Set : A:\M-2335p1.app

Output Set: N:\CRF3\01162002\J032254.raw

129 <212> TYPE: DNA
 130 <213> ORGANISM: Artificial Sequence
 132 <220> FEATURE:
 133 <223> OTHER INFORMATION: Description of Artificial Sequence:degenerate
 134 oligonucleotide primer PTKIa
 136 <400> SEQUENCE: 3 *→ see item 9 on Enr Summary Sheet*
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 143 <213> ORGANISM: Artificial Sequence
 145 <220> FEATURE:
 146 <223> OTHER INFORMATION: Description of Artificial Sequence:degenerate
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 169 <213> ORGANISM: Artificial Sequence
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 180 <211> LENGTH: 1412
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 182 <213> ORGANISM: Homo sapiens
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 187 gtggccctca agtgcattcc caagaaggcc ctccggggca aggaggccct ggtggagaac 180
 188 gagatcgcag tgctccgtag gatcagtcac cccaacatcg tcgctctgga ggatgtccac 240
 189 gatagccctt cccacctcta cctggccatg gaactggtga cgggtggcga gctgtttgac 300
 190 cgcattcatgg agcgcggctc ctacacagag aaggatgccg gccatctggt gggtcaggtc 360
 191 cttggcgccg tctcctacct gcacagcctg gggatcgtgc accgggacct caagcccga 420
 192 aacctcctgt atgccacgcc ctttgaggac tcgaagatca tggctctctga ctttgactc 480
 193 tccaaaatcc aggtctggaa catgctaggc accgcctgtg ggaccctgg atatgtggc 540
 194 ccagagctct tggagcagaa accctacggg aaggccgtag atgtgtgggc cctgggcgtc 600

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Input Set : A:\M-2335p1.app

Output Set: N:\CRF3\01162002\J032254.raw

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195 atctcctaca tctgctgtg tgggtacccc cccttctacg acgagagcga cctgagctc 660
196 ttcagccaga tctgagggc cagctatgag tttgactctc ctttctggga tgacatctca 720
197 gaatcagcca aagacttcat ccggcacctt ctggagcgag acccccagaa gaggttcacc 780
198 tgccaacagg ccttgccgca cctttggatc tctggggaca cagccttcga cagggacatc 840
199 ttaggctctg tcagtggca gatccggaag aactttgctc ggacacactg gaagcgagcc 900
200 ttcaatgcca cctcgttcct gcgccacatc cggaagctgg gccagatccc agagggcgag 960
201 ggggcctctg agcagggcat ggcccgccac agccactcag gcctccgtgc tggccagccc 1020
202 cccaagtggg gatgccagg cagatgccga ggccaagtgg actgaccccc agatttcctt 1080
203 ccttggtatg ctttcggtcc cctcccccaa cccctcccc tgggtctggc ctctgctgga 1140
204 ttttgagatt tgaggggtg gcgcatggcg ctggggttgg aatggggcac cccaagtct 1200
205 gtccccaggc tctgccctgc ctgggggcag tggctccctt cccctgttgc ctctcccgcc 1260
206 cctgcccccc ccgccccgcc aaaagccgag ggggtgctgg caggcgggccc tcaggggctg 1320
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212 <211> LENGTH: 343
213 <212> TYPE: PRT
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218 1 5 10 15
220 Ile Arg Glu Arg Leu Gly Ser Gly Ala Phe Ser Glu Val Val Leu Ala
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223 Gln Glu Arg Gly Ser Ala His Leu Val Ala Leu Lys Cys Ile Pro Lys
224 35 40 45
226 Lys Ala Leu Arg Gly Lys Glu Ala Leu Val Glu Asn Glu Ile Ala Val
227 50 55 60
229 Leu Arg Arg Ile Ser His Pro Asn Ile Val Ala Leu Glu Asp Val His
230 65 70 75 80
232 Glu Ser Pro Ser His Leu Tyr Leu Ala Met Glu Leu Val Thr Gly Gly
233 85 90 95
235 Glu Leu Phe Asp Arg Ile Met Glu Arg Gly Ser Tyr Thr Glu Lys Asp
236 100 105 110
238 Ala Ser His Leu Val Gly Gln Val Leu Gly Ala Val Ser Tyr Leu His
239 115 120 125
241 Ser Leu Gly Ile Val His Arg Asp Leu Lys Pro Glu Asn Leu Leu Tyr
242 130 135 140
244 Ala Thr Pro Phe Glu Asp Ser Lys Ile Met Val Ser Asp Phe Gly Leu
245 145 150 155 160
247 Ser Lys Ile Gln Ala Gly Asn Met Leu Gly Thr Ala Cys Gly Thr Pro
248 165 170 175
250 Gly Tyr Val Ala Pro Glu Leu Leu Glu Gln Lys Pro Tyr Gly Lys Ala
251 180 185 190
253 Val Asp Val Trp Ala Leu Gly Val Ile Ser Tyr Ile Leu Leu Cys Gly
254 195 200 205
256 Tyr Pro Pro Phe Tyr Asp Glu Ser Asp Pro Glu Leu Phe Ser Gln Ile
257 210 215 220
259 Leu Arg Ala Ser Tyr Glu Phe Asp Ser Pro Phe Trp Asp Asp Ile Ser
260 225 230 235 240

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Output Set: N:\CRF3\01162002\J032254.raw

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262 Glu Ser Ala Lys Asp Phe Ile Arg His Leu Leu Glu Arg Asp Pro Gln
263                245                250                255
265 Lys Arg Phe Thr Cys Gln Gln Ala Leu Arg His Leu Trp Ile Ser Gly
266                260                265                270
268 Asp Thr Ala Phe Asp Arg Asp Ile Leu Gly Ser Val Ser Glu Gln Ile
269                275                280                285
271 Arg Lys Asn Phe Ala Arg Thr His Trp Lys Arg Ala Phe Asn Ala Thr
272                290                295                300
274 Ser Phe Leu Arg His Ile Arg Lys Leu Gly Gln Ile Pro Glu Gly Glu
275 305                310                315                320
277 Gly Ala Ser Glu Gln Gly Met Ala Arg His Ser His Ser Gly Leu Arg
278                325                330                335
280 Ala Gly Gln Pro Pro Lys Trp
281                340
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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/032,254

DATE: 01/16/2002

TIME: 18:43:56

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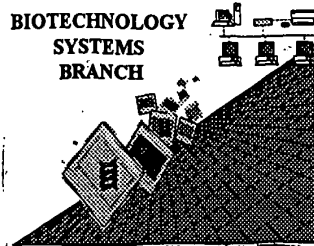
Output Set: N:\CRF3\01162002\J032254.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:137 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:137 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:137 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/032,254
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.	
10 _____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

01 0/0420 025



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/032,254
Source: 01P6
Date Processed by STIC: 1/16/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)

2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202

3. Hand Carry directly to:

U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202

Or

U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202